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1

#8

SEQUENCE LISTING

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<120> Regulation of Angiogenesis With Zinc
Finger Proteins

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<150> US 09/733,604

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Arg Ser Asp Ala Leu Ala Arg
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Lys Thr Ser His Leu Arg Ala
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<210> 171

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Met Ser His His Leu Ser Arg
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Arg Ser Asp His Leu Ser Arg
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Arg Ser Asp Asn Leu Ala Arg
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<400> 181
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18

<210> 183
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<220>
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<400> 183
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19

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<400> 184
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9

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<210> 188
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<220>
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 Glu Arg Gly Asp Leu Thr Arg
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<210> 189
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Asp Arg Ser Asn Leu Thr Arg
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Arg Ser Asp Ala Leu Thr Gln
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Asp Arg Ser Asn Leu Thr Arg
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<210> 199

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<400> 199

Met Ser His His Leu Ser Arg
1 5

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1           5

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      <220>
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      <400> 201
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1           5

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      <220>
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      <400> 202
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1           5

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      <220>
      <223> recognition helix

      <400> 203
Gln Ser Ser Asp Leu Thr Arg
1           5

      <210> 204
      <211> 20
      <212> DNA
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      <220>
      <223> VEGF-C forward primer

      <400> 204
tgccgatgca tgtctaaact

      <210> 205
      <211> 22
      <212> DNA
      <213> Artificial Sequence

      <220>

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<223> VEGF-C reverse primer

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tgaacagggtc tcttcatcca gc 22

<210> 206
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<220>
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<221> modified_base
<222> (26)...(26)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 206
nagcaacact accacagtgt caggcn 26

<210> 207
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> target

<400> 207
tgagcggcgg cagcggagc 19

<210> 208
<211> 25
<212> PRT
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<220>
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class of zinc finger proteins (ZFP)

<221> MOD_RES
<222> (2)...(5)
<223> Xaa = any amino acid, Xaa in positions 4 and 5 may
be present or absent

<221> MOD_RES
<222> (7)...(18)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (20)...(24)
<223> Xaa = any amino acid, Xaa in positions 23 and 24
may be present or absent

<400> 208
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

1 5 10 15
 Xaa Xaa His Xaa Xaa Xaa Xaa His
 20 25

<210> 209
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 <212> DNA
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<220>
 <223> target

<400> 209
 ggcgtagac

9

<210> 210
 <211> 9
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<220>
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<400> 210
 ggcgacgta

9

<210> 211
 <211> 5
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<220>
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<400> 211
 Thr Gly Glu Lys Pro
 1 5

<210> 212
 <211> 5
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<220>
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<400> 212
 Gly Gly Gly Gly Ser
 1 5

<210> 213
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<220>
 <223> peptide linker

<400> 213
 Gly Gly Arg Arg Gly Gly Gly Ser
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<210> 214
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<210> 215
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<400> 215
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<210> 216
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<220>
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<400> 216
 Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
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<210> 217
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<220>
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 factor Zif268

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 Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
 20 25 30

<210> 218
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<220>
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 factor Zif268

<400> 218
 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
 1 5 10 15
 Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
 20 25

<210> 219
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<220>
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 factor Zif268

<400> 219
 Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg
 1 5 10 15
 Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
 20 25

<210> 220
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<220>
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<400> 220
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9

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<220>
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<400> 221
 Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly Lys
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 Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp His Thr
 20 25 30
 Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe
 35 40 45
 Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr Gly Glu
 50 55 60
 Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp
 65 70 75 80
 His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly
 85 90

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<210> 223
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 <223> Sp-i consensus sequence with leader sequence

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 Met Glu Lys Leu Arg Asn Gly Ser Gly Asp Pro Gly Lys Lys Lys Gln
 1 5 10 15
 His Ala Cys Pro Glu Cys Gly Lys Ser Phe Ser Lys Ser Ser His Leu
 20 25 30
 Arg Ala His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro
 35 40 45
 Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Gln Arg His Gln
 50 55 60
 Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
 65 70 75 80
 Ser Phe Ser Arg Ser Asp His Leu Ser Lys His Gln Arg Thr His Gln
 85 90 95
 Asn Lys Lys Gly
 100

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 large T antigen

<400> 224
 Pro Lys Lys Lys Arg Lys Val
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<210> 225
 <211> 8
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<220>
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<400> 225
 Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 226
 <211> 21
 <212> DNA
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<220>
 <223> VEGF-A forward primer

<400> 226
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<210> 227
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 <212> DNA
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<220>
 <223> VEGF-A reverse primer

<400> 227
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<210> 228
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<221> modified_base
 <222> (25)...(25)
 <223> n = a modified by tetramethylrhodamine (TAMRA)

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<220>
 <223> GAPDH forward primer

<400> 229
 ccatgttcgt catgggtgtg a 21

<210> 230
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 <212> DNA
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<220>
 <223> GAPDH reverse primer

<400> 230
 catggactgt ggtcatgagt 20

<210> 231
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<220>

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<223> GAPDH Taqman probe

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<221> modified_base
<222> (24)...(24)
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<220>
<223> VP16-FLAG forward primer

<400> 232
catgacgatt tcgatctgga                                         20

<210> 233
<211> 22
<212> DNA
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<220>
<223> VP16-FLAG reverse primer

<400> 233
ctacttgatca tcgtcgctcct tg                                    22

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<220>
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<223> n = a modified by aminofluorescein (FAM)

<221> modified_base
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<223> RT-PCR primer

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28

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<220>
<223> RT-PCR primer

<400> 236
tcaccgcctc ggcttgtcac at

22

<210> 237
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<220>
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18

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<220>
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Arg Ser Asp Glu Leu Ser Arg
1 5

<210> 239
<211> 7
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<220>
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<400> 239
Gln Ser Gly His Leu Thr Lys
1 5

<210> 240
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<213> Artificial Sequence

<220>
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<400> 240
gctgggggag

10

<210> 241
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<220>
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<400> 241
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49

<210> 242
 <211> 37
 <212> DNA
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<220>
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<400> 242
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37

<210> 243
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<210> 244
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<220>
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<220>
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<400> 245
 Thr Ser Gly His Leu Thr Arg
 1 5

<210> 246

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 Thr Ser Gly His Leu Ile Arg
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 Thr Ser Gly His Leu Ser Arg
 1 5

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<400> 248
 Thr Ser Gly His Leu Ala Arg
 1 5

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<400> 249
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<400> 250
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 1 5

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Thr Thr Gly His Leu Val Arg
1 5

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Thr Lys Asp His Leu Val Arg
1 5